SEQUENCE LISTING

<110> Michael S.C. Fung
Bill N.C. Sun
Cecily R.Y. Sun

<120> Inhibitors of Complement Activation

<130> 98-2A

<150> 60/075,328
<151> 1998-02-20

<150> 09/253,689
<151> 1999-02-20

<160> 15

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 699
<212> DNA
<213> human

<220>
<221> CDS
<222> (4)...(687)

<400> 1

```
cgg atc ctg ggc ggc aga gag gcc gag gcg cac gcg cgg ccc tac atg      48
   Ile Leu Gly Gly Arg Glu Ala Glu Ala His Ala Arg Pro Tyr Met
    1               5                  10                  15

gcg tcg gtg cag ctg aac ggc gcg cac ctg tgc ggc ggc gtc ctg gtg      96
Ala Ser Val Gln Leu Asn Gly Ala His Leu Cys Gly Gly Val Leu Val
                20                  25                  30

gcg gag cag tgg gtg ctg agc gcg gcg cac tgc ctg gag gac gcg gcc     144
Ala Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Ala Ala
            35                  40                  45

gac ggg aag gtg cag gtt ctc ctg ggc gcg cac tcc ctg tcg cag ccg     192
Asp Gly Lys Val Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro
        50                  55                  60

gag ccc tcc aag cgc ctg tac gac gtg ctc cgc gca gtg ccc cac ccg     240
Glu Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro
    65                  70                  75

gac agc cag ccc gac acc atc gac cac gac ctc ctg ctg cta cag ctg     288
Asp Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Leu Gln Leu
```

80 85 90 95

tcg gag aag gcc aca ctg ggc cct gct gtg cgc ccc ctg ccc tgg cag 336
Ser Glu Lys Ala Thr Leu Gly Pro Ala Val Arg Pro Leu Pro Trp Gln
100 105 110

cgc gtg gac cgc gac gtg gca ccg gga act ctc tgc gac gtg gcc ggc 384
Arg Val Asp Arg Asp Val Ala Pro Gly Thr Leu Cys Asp Val Ala Gly
115 120 125

tgg ggc ata gtc aac cac gcg ggc cgc cgc ccg gac agc ctg cag cac 432
Trp Gly Ile Val Asn His Ala Gly Arg Arg Pro Asp Ser Leu Gln His
130 135 140

gtg ctc ttg cca gtg ctg gac cgc gcc acc tgc aac cgg cgc acg cac 480
Val Leu Leu Pro Val Leu Asp Arg Ala Thr Cys Asn Arg Arg Thr His
145 150 155

cac gac ggc gcc atc acc gag cgc ttg atg tgc gcg gag agc aat cgc 528
His Asp Gly Ala Ile Thr Glu Arg Leu Met Cys Ala Glu Ser Asn Arg
160 165 170 175

cgg gac agc tgc aag ggt gac tcc ggg ggc ccg ctg gtg tgc ggg ggc 576
Arg Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly
180 185 190

gtg ctc gag ggc gtg gtc acc tcg ggc tcg cgc gtt tgc ggc aac cgc 624
Val Leu Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg
195 200 205

aag aag ccc ggg atc tac acc cgc gtg gcg agc tat gcg gcc tgg atc 672
Lys Lys Pro Gly Ile Tyr Thr Arg Val Ala Ser Tyr Ala Ala Trp Ile
210 215 220

gac agc gtc ctg gcc tagtaggaat tc 699
Asp Ser Val Leu Ala
225

<210> 2
<211> 228
<212> PRT
<213> human

<400> 2
Ile Leu Gly Gly Arg Glu Ala Glu Ala His Ala Arg Pro Tyr Met Ala
1 5 10 15
Ser Val Gln Leu Asn Gly Ala His Leu Cys Gly Gly Val Leu Val Ala
20 25 30
Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Ala Ala Asp
35 40 45
Gly Lys Val Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro Glu
50 55 60
Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro Asp
65 70 75 80

Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Leu Gln Leu Ser
85 90 95
Glu Lys Ala Thr Leu Gly Pro Ala Val Arg Pro Leu Pro Trp Gln Arg
100 105 110
Val Asp Arg Asp Val Ala Pro Gly Thr Leu Cys Asp Val Ala Gly Trp
115 120 125
Gly Ile Val Asn His Ala Gly Arg Arg Pro Asp Ser Leu Gln His Val
130 135 140
Leu Leu Pro Val Leu Asp Arg Ala Thr Cys Asn Arg Arg Thr His His
145 150 155 160
Asp Gly Ala Ile Thr Glu Arg Leu Met Cys Ala Glu Ser Asn Arg Arg
165 170 175
Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val
180 185 190
Leu Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg Lys
195 200 205
Lys Pro Gly Ile Tyr Thr Arg Val Ala Ser Tyr Ala Ala Trp Ile Asp
210 215 220
Ser Val Leu Ala
225

<210> 3
<211> 714
<212> DNA
<213> pig

<220>
<221> CDS
<222> (4)...(702)

<400> 3
cgg atc ctg ggt ggc cag gag gcc aag tcc cac gag aga ccc tac atg 48
Ile Leu Gly Gly Gln Glu Ala Lys Ser His Glu Arg Pro Tyr Met
1 5 10 15

gca tcg gtg cag gtg aac ggc aag cac gtg tgc gga ggc ttc ctg gtg 96
Ala Ser Val Gln Val Asn Gly Lys His Val Cys Gly Gly Phe Leu Val
20 25 30

tct gag cag tgg gtg ctg agt gca gca cac tgc ctg gag gac gtg gcc 144
Ser Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Val Ala
35 40 45

gag ggg aag ctg cag gtt ctc ctg ggt gcg cac tcc ctg tca cag ccc 192
Glu Gly Lys Leu Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro
50 55 60

gag ccc tcg aag cgc ctg tac gac gtg ctc cgc gcc gtg ccc cac cca 240
Glu Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro
65 70 75

gac agc cag cct gac acc atc gac cat gat ctc ctc ctg ctg aag ctc 288
Asp Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Leu Lys Leu
80 85 90 95

tcc gag aag gcc gag ctg ggc cct gcc gtg cag ccc ctt gcc tgg caa 336
Ser Glu Lys Ala Glu Leu Gly Pro Ala Val Gln Pro Leu Ala Trp Gln
100 105 110

cga gag gac cac gag gtt ccg gca ggc acg ctc tgc gac gtg gcc ggc 384
Arg Glu Asp His Glu Val Pro Ala Gly Thr Leu Cys Asp Val Ala Gly
115 120 125

tgg gga gtg gtc agt cac act ggc cgc cgg ccc gac cgt ctg cag cac 432
Trp Gly Val Val Ser His Thr Gly Arg Arg Pro Asp Arg Leu Gln His
130 135 140

ctg ctc cta ccg gtg ctg gac cgc acc acc tgc aac ctg cgc aca tac 480
Leu Leu Leu Pro Val Leu Asp Arg Thr Thr Cys Asn Leu Arg Thr Tyr
145 150 155

cac gat ggc acc atc acc gag cgc atg atg tgc gcg gag agc aac cgt 528
His Asp Gly Thr Ile Thr Glu Arg Met Met Cys Ala Glu Ser Asn Arg
160 165 170 175

cgg gac agc tgc aag ggc gac tcc gga ggc ccg ctg gtg tgc ggg ggt 576
Arg Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly
180 185 190

gtg gcc gag gga gtg gtt acc tca ggc tcc cga gtc tgc ggc aac cgc 624
Val Ala Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg
195 200 205

aag aaa ccc ggc atc tac acg cgc ttg gcg agc tac gtg gcc tgg atc 672
Lys Lys Pro Gly Ile Tyr Thr Arg Leu Ala Ser Tyr Val Ala Trp Ile
210 215 220

gac gga gtg atg gct gac agc gca gcc gcc tagtaggaat tc 714
Asp Gly Val Met Ala Asp Ser Ala Ala Ala
225 230

<210> 4
<211> 233
<212> PRT
<213> pig

<400> 4
Ile Leu Gly Gly Gln Glu Ala Lys Ser His Glu Arg Pro Tyr Met Ala
1 5 10 15
Ser Val Gln Val Asn Gly Lys His Val Cys Gly Gly Phe Leu Val Ser
20 25 30
Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Val Ala Glu
35 40 45
Gly Lys Leu Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro Glu
50 55 60
Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro Asp
65 70 75 80
Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Leu Lys Leu Ser
85 90 95

Glu Lys Ala Glu Leu Gly Pro Ala Val Gln Pro Leu Ala Trp Gln Arg
100 105 110
Glu Asp His Glu Val Pro Ala Gly Thr Leu Cys Asp Val Ala Gly Trp
115 120 125
Gly Val Val Ser His Thr Gly Arg Arg Pro Asp Arg Leu Gln His Leu
130 135 140
Leu Leu Pro Val Leu Asp Arg Thr Thr Cys Asn Leu Arg Thr Tyr His
145 150 155 160
Asp Gly Thr Ile Thr Glu Arg Met Met Cys Ala Glu Ser Asn Arg Arg
165 170 175
Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val
180 185 190
Ala Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg Lys
195 200 205
Lys Pro Gly Ile Tyr Thr Arg Leu Ala Ser Tyr Val Ala Trp Ile Asp
210 215 220
Gly Val Met Ala Asp Ser Ala Ala Ala
225 230

<210> 5
<211> 25
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 5
tgcggccgct gtaggtgctg tcttt 25

<210> 6
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 6
ggaattcact cgttattctc gga 23

<210> 7
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 7
tccgagaata acgagtg 17

<210> 8
<211> 29
<212> DNA

<213> Artificial Sequence

<220>
<223> primer

<400> 8
cattgaaagc tttggggtag aagttgttc 29

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 9
cgcggccgca gctgctcaga gtgtaga 27

<210> 10
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 10
cggtaagctt cactggctca gggaaata 28

<210> 11
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 11
aagaagcttg ccgccaccat ggattggctg tggaact 37

<210> 12
<211> 31
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 12
cgggatcctc aaactttctt gtccaccttg g 31

<210> 13
<211> 36
<212> DNA

<213> Artificial Sequence

<220>
<223> primer

<400> 13
aagaaagctt gccgccacca tgttctcact agctct 36

<210> 14
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 14
cgggatcctt ctccctctaa cactct 26

<210> 15
<211> 9
<212> PRT
<213> human

<400> 15
Glu Pro Lys Ser Cys Asp Lys Thr His
1 5